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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/302,863

DATE: 09/03/1999  
TIME: 10:56:44

Input Set: I302863.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1  <110> APPLICANT: Goodwin, Raymond G
2      Din, Wanwan S.
3  <120> TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
4  <130> FILE REFERENCE: 2519
5  <140> CURRENT APPLICATION NUMBER: US/09/302,863
6  <141> CURRENT FILING DATE: 1999-04-30
7  <160> NUMBER OF SEQ ID NOS: 5
8  <170> SOFTWARE: PatentIn Ver. 2.0
9  <210> SEQ ID NO 1
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12 <213> ORGANISM: Human
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20      agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg      97
21      Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
22              15              20              25
23      gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg      145
24      Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
25              30              35              40
26      ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc      193
27      Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
28              45              50              55              60
29      acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc      241
30      Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
31              65              70              75
32      aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc      289
33      Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
34              80              85              90
35      tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc      337
36      Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
37              95              100              105
38      agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga      385
39      Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
40              110              115              120
41      gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag      433
42      Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu
43              125              130              135              140
44      cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt      481

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45      His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
46                      145                      150                      155
47      gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt      529
48      Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
49                      160                      165                      170
50      gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag      577
51      Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
52                      175                      180                      185
53      agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt      625
54      Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
55                      190                      195                      200
56      ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg      673
57      Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
58      205                      210                      215                      220
59      agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag      721
60      Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
61                      225                      230                      235
62      tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac      769
63      Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
64                      240                      245                      250
65      ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg      817
66      Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
67      255                      260                      265
68      cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg      865
69      Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
70      270                      275                      280
71      cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg      912
72      Pro Ala Gln Glu Gly Gly Pro Gly Ala
73      285                      290
74      aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972
75      gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032
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80      gcaataaagt cctcgtgcct gctgetcaca gcccccgaga gcccctcctc ctggagaata 1332
81      aaacctttgg cagctgccct tcctcaaaaa aaaaaaaaaa aaaaa      1377
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89      Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
90      20                      25                      30
91      Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
92      35                      40                      45
93      Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
94      50                      55                      60

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95      Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
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97      His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
98              85              90              95
99      Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100              100              105              110
101      Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
102              115              120              125
103      Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
104              130              135              140
105      Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
106              145              150              155              160
107      Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
108              165              170              175
109      Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
110              180              185              190
111      Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
112              195              200              205
113      Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
114              210              215              220
115      Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
116      225              230              235              240
117      Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
118              245              250              255
119      Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
120              260              265              270
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134      atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt      105
135      Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
136      1              5              10              15
137      aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca      153
138      Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
139              20              25              30
140      cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg      201
141      Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
142              35              40              45
143      gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg      249
144      Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val

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145          50          55          60
146      tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg      297
147      Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
148          65          70          75          80
149      gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga      345
150      Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
151          85          90          95
152      gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg      393
153      Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
154          100          105          110
155      aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac      441
156      Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
157          115          120          125
158      agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa      489
159      Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
160          130          135          140
161      gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa      537
162      Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
163          145          150          155          160
164      gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt      585
165      Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
166          165          170          175
167      gcc cta gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac      633
168      Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
169          180          185          190
170      ttt ttt ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg      681
171      Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
172          195          200          205
173      gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg      729
174      Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
175          210          215          220
176      agt ctg gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta      777
177      Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
178          225          230          235          240
179      ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga      825
180      Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
181          245          250          255
182      gat gaa ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg      873
183      Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
184          260          265          270
185      gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt      922
186      Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
187          275          280          285
188      acaccatgtc tgtagctatt ttctccctt tctctgtacc tctaagaaga aagaatctaa      982
189      ctgaaaatac caaaaaaaaaa aaaaaaaaaa aaagatcttt aattaagcgg ccgcaagctt      1042
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193 <212> TYPE: PRT
194 <213> ORGANISM: Human

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198 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
199 20 25 30
200 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
201 35 40 45
202 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
203 50 55 60
204 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
205 65 70 75 80
206 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
207 85 90 95
208 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
209 100 105 110
210 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
211 115 120 125
212 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
213 130 135 140
214 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
215 145 150 155 160
216 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
217 165 170 175
218 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
219 180 185 190
220 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
221 195 200 205
222 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
223 210 215 220
224 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225 225 230 235 240
226 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
227 245 250 255
228 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
229 260 265 270
230 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
231 275 280 285
232 <210> SEQ ID NO 5
233 <211> LENGTH: 232
234 <212> TYPE: PRT
235 <213> ORGANISM: human
236 <400> SEQUENCE: 5
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238 1 5 10 15
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240 20 25 30
241 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
242 35 40 45
243 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
244 50 55 60

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**VERIFICATION SUMMARY**  
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